### SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: TANABE, Tadashi
  - (ii) TITLE OF INVENTION: PROSTACYCLIN SYNTHASE DERIVED FROM HUMAN
  - (iii) NUMBER OF SEQUENCES: 17
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
    - (B) STREET: 2100 Pennsylvania Avenue, N.W.
    - (C) CITY: Washington
    - (D) STATE: D.C.
    - (E) COUNTRY: USA
    - (F) ZIP: 20037
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 08/578,709
      - (B) FILING DATE: 28-DEC-1995
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: PCT/JP95/00838
    - (B) FILING DATE: 27-APR-1995
    - (vii) PRIOR APPLICATION DATA:
      - (A) APPLICATION NUMBER: JP 114316/1994
        - (B) FILING DATE: 28-APR-1994
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Gubinsky, Louis
    - (B) REGISTRATION NUMBER: 24,835 (C) REFERENCE/DOCKET NUMBER: 040439
    - (C) REFERENCE/DOCKET NUMBER: Q4043
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (202)293-7060
    - (B) TELEFAX: (202)293-7860
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 16 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid

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(A)	DESCRIPTION: /des	c =	"PRI	MER/SYN	THETE	C DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
GGGACAAGGA CCACAT	16
(2) INFORMATION FOR SEQ LD NO:2:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	1
(ii) MOLECULE TYPE: other nucleic acid	
(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
CAAAAGTCGC, CTGTGGAAGC	20
CAMMOTOC CIGIOGRAGE	20
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 18 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other nucleic acid	
(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"	
그는 지하는 물건으로 가입하다는 사람들은 그리를 가지 않는다.	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
(XI) SEQUENCE DESCRIPTION. SEQ ID NO.3.	
CACAGGCGAC TTTTGACA	18
(2) INFORMATION FOR SEQ ID NO:4:	
(1) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 18 base pairs (B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: other nucleic acid	
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TGCCTGCATC TCCTCTGA  18  (2) INFORMATION FOR SEQ ID NO:5:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  GACTCGAGTC GACATCGATT TTTTTTTTT TTTTT  (2) INFORMATION FOR SEQ ID NO:6:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (i) MOLECULE TYPE: other nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
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(D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  GACTCGAGTC GACATCGATT TTTTTTTTT TTTTT  (2) INFORMATION FOR SEQ ID NO:6:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
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(8) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	(i	) SEQU	ENCE CHARA	CTERISTICS:		*		
(C) STRANDENNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (i) LENGTH: 48 base pairs (ii) TYPE: nucleic acid (c) STRANDEDNESS: single (d) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
(D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"		(D)	TOPOLOGY	linear				
(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDMESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid  (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	13.4	MOTE	CITE TVDE	other nucl	aig agid			
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (i) LENGTH: 48 base pairs (ii) TYPE: nucleic acid (c) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	, , , , , , , , , , , , , , , , , , , ,					THETTC DNA		
GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"		1						
GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"			9 - 6					
GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"		119						
GACTCGAGTC GACATCG  (2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	1 45.			1	2 2 2			
(2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	(xi	) SEQU	JENCE DESCI	RIPTION: SEQ	ID NO:6:			
(2) INFORMATION FOR SEQ ID NO:7:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDMESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid  (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	CACTCCA	ana ar	CATCG					17
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	GACICGA	GIC GA	CAICG					+1
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 48 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid  (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	(2) INF	ORMATI	ON FOR SEC	O ID NO:7:				
(A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANNENNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	(0)							
(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	.(i	) SEQU	JENCE CHAR	ACTERISTICS:				
(C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"					s			
(D) TOPOLOGY: linear  (ii) MOLECULE TYPE: other nucleic acid  (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
(ii) MOLECULE TYPE: other nucleic acid (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"								
(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"		(D)	TOPOLOGY	: 11near				
(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC RNA"	1::	) MOT	פמעים שוווים:	other much	eic acid			
	(11					THETTC RNA	, n	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:		. (41)	PUDCKIFI	,	- KINDA, OII	The state of the s		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:		7-						
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:								4.5
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	1 1							
	(xi	) SEQU	JENCE DESC	RIPTION: SEQ	ID NO:7:			

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- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 183 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
    - (vi) ORIGINAL SOURCE:
      - ORIGINAL SOURCE:
        - (A) ORGANISM: Homo sapiens (B) STRAIN: lambda hPGIS141
    - (ix) FRATURE:
      - (A) NAME/KEY: CDS
        - (B) LOCATION: 1..183
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
- GGG GAC AAG GAC CAC ATG TGC AGT GTC AAA AGT CGC CTG TGG AAG CTG Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu
- CTA TCC CCA GCC AGG CTG GCC AGG GCC CAC CGG AGC AAA TGG CTG 96
  Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu
- GAG AGT TAC CTG CTG CAC CTG GAG GAG ATG GGT GTG TCA GAG GAG ATG
  Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met
  35
  46
  47
- CAG GCA CGG GCC CTG GTG CTG CAG CTG TGG GCC ACA CAG
  Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln
  50
- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 61 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu 1 5 10 15

Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu 20 25 30

1.	(ii)	MOL	ECUL	E TY	PE:	CDNA			-								
		1 Y													14		
	(vi)	ORI						-								á.	
			OR					iens									217
	1	(E	) SI	RAIN	: pH	PGIS	36										
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	(ix)	FEF									1					,	
			NA														
		. (E	F) F	CATI	ON:	80.	790								. 1		
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1	(ix)	FEF			4.1								1				
			A) NA														
		(E	3) LC	ÇAŢI	ON:	80.	790								100		
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. 4	(xi)	SEC	QUENC	CE DE	SCR	PTIC	N: 5	EQ 1	ID NO	0:10:	:						
				5 -													
CTAC	TAC	rac 1	CAGGO	CACC	C G	CCA	TAG	ACC	GGGG	GGGG	GGGG	GGGG	GGG (	GCAG	CCCG	C	60
, ÷.																	
CAGO	CCCC	GCC I	AGCCC	CCGCC											GCC		112
	. *	÷ ' '			Met	: Ala	Tr	Ala	a Al	a Lei	ı Leı	ı Gl	Lei		ı Ala		
					3	L.			. :	5				10	)		
			٠									1					100
										CGC							160
Ala	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Arg	Arg	Arg	Thr	Arg	Arg	Pro		
			15					20				1.2	25				
							1			15.						1	
										CĊC						٠	208
Gly	Glu		Pro	Leu	Asp	Leu	Gly	Ser	Ile	Pro.	Trp	Leu	Gly	Tyr	Ala		
		30					35		- :			40					4.
										CTC							256
Leu	Asp	Phe	Gly	Lys	Asp	Ala	Ala	Ser	Phe	Leu	Thr	Arg	Met	Lys	·Glu		4
	45					50				- "	55						
										GGG							304
	His	Gly	Asp	Ile	Phe	Thr	Ile	Leu	Val	Gly	Gly	Arg	Tyr	Val			
60		2.7			65					70					75		
										2.				;			. *
										GTG							352
Val	Leu	Leu	Asp	Pro	His	Ser	Tyr	Asp	Ala	Val	Val	Trp	G1u				
				80					. 85	- 5				90			
						A1.										į.	

Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 792 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear:

AĊC	AGG	CTC	GAC	TTC	CAT	GCC	TAT	GCC	ATC	TTC	CTC	ATG	GAG	AGG	ATT		400
Thr	Arg	Leu	Asp.	Phe	His	Ala	Tyr	Ala	Ile	Phe	Leu	Met	Glu	Arg	Ile		
			95					100					105			1	
								· .		11							
TŢT	GAT	GTG	CAG	CTT	CCA	ÇĄT	TAC	AGC	CCC	AGT	GAT	GAA	AAG	GCC	AGG	1.0	448
Phe	Asp	Val	Gln	Leu	Pro	His	Tyr	Ser	Pro	ser	Asp	Glu	Lys	Äla	Arg		
		110					115					120					
															GCC	5	496
Met	Lys	Leu	Thr	Leu	Leu	His	Arg	Glu	Leu	Gln	Ala	Leu	Thr	Glu	Ala		14 Lat.
	125		*			130					135						
	7 -	- 10		. "						1.5						1 × 4.	
															GCA		544-
Met	Tyr.	Thr	Asn	Leu	His	Ala	Val	Leu	Leu	Gly	Asp	Ala	Thr	Glu	Ala		- 30
140					145	- 1				150					155		1
						1 1	4			1.							
				CAC													592
Gly	Ser	Gly	Trp	His	Glu	Met	Gly	Leu	Leu	Asp	Phe	Ser	Tyr	Ser	Phe	1.5	15
e		2.		160		5.1		1 2	165				* ' '	170		. 7	
1		4 1 1	3	-	1. 3.	1, 10,					12.2	13			4-	1	
				GGC													640
Leu	Leu	Arg	Ala.	Gly	Tyr	Leu	Thr		Tyr	GLY	lle	G1u		Leu	Pro		L. 19
			175					180		1 2	- 50		185			3.1	1 1
		خلا	1.1			422		~~~		aimia	~ ~		~~~	114	-		
															GTC		688
Arg	Thr		GIU	ser	Gin	Ата		vėb	Arg	vai	His		ALA	Asp	Val.		
		190					195				1	200					
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				CGC												1.	.736
Pne		Inr	Pne	Arg	GIN	210	АБР	Arg	ren.	Leu	PEO	rys	Leu,	Ala	Arg	10	
	205					210					415	1.50			4,		
-	maa	omo	man	GTG	900	a.a		0.00	and.	n ma	maa	N CIT	oma	***	a com		784
				Val												4	784
	ser	Leu	ser	val	225	Asp	гув	Asp	uls	230	Cys	ser	val	μλg	235		
220					225	21				230					235		
aaa	ama	ma			- 1						***	41	1				700
	CTG	16						* , '			7						792
arg	Leu			419		7.3		1.2		0.0							

### (2) INFORMATION FOR SEO ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 237 amino acids
  - (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala Ala Leu Leu Leu Leu 1 5 10 15

Leu Leu Leu Ser Arg Arg Arg Thr Arg Arg Pro Gly Glu Pro Pro Leu

Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala Leu Asp Phe Gly Lys

Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu Lys His Gly Asp Ile

Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr Val Leu Leu Asp Pro

His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg Thr Arg Leu Asp Phe-

His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile Phe Asp Val Gln Leu

Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg Met Lys Leu Thr Leu 115

Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala Met Tyr Thr Asn Leu

His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala Gly Ser Gly Trp His 155 150

Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe Leu Leu Arg Ala Gly 170

Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser 185

Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg

Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg Gly Ser Leu Ser Val 215

Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu 230

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1296 base pairs (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

# (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
  - (B) STRAIN: pHPGIS135
- (ix) FEATURE:
  - (A) NAME/KEY: CDS

## (B) LOCATION: 3..827

# (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 3..827

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	(202)	, 92.	202					, ,			•						
GG G	GAC /	AAG .	GÁC (	CAC I	ATG :	rge z	AGT (	TC I	AAA A	AGT (	CGC (	CTG	rgg i	AAG (	CTG		47
.1	Asp I	Lys i	Asp I	lis I	let (	Cys S	Ser V	Val 1	Lys	Ser 1	Arq 1	Leu '	Trp 1	Lys I	Leu		
	1	· ; *			- 5	-	**		•	10	-		•	•	15		
-	4		. :	1.							*						
CTA	TCC	CCA	GCC	AGG	CTG	GCĊ	ÁGG	CGG	GCC	CAC	CGG	AGC	AAA	TGG	CTG.		95
Leu	Ser	Pro	Ala	Arq	Leu	Ala	Arg	Arg	Ala	His	Arg	Ser	Lys	Trp	Leu		
1.				- 20			- 5	-	25		-		٠.	30			
															- 1		
GAG	AGT	TAC	CTG	CTG	CAC	CTG	GAG	GAG	ATG	GGT	GTG	TCA	GAG	GAG	ATG		143
Glu	Ser	Tyr	Leu	Leu	His	Leu	Glu	Glu	Met	Gly	Val	Ser	Glu	Glu	Met		
1			35					40			n is		45				
	-, 4																
CAG	GCA	CGG	GCC	CTG	GTG	CTG	CAG	CTG	TGG	GCC	ACA	CAG	GGG	AAT	ATG		.191
Gln	Ala	Arg	Ala	Leu	Val	Leu	Gln	Leu	Trp	Ala	Thr	Gln	Gly	Asn	Met		
	14	50		,		9 .	55					60		100			
									, ,								
GGT	CCC	GCT	GCC	TTC	TGG	CTC	CTG	CTC	TŢĊ	CTT	CTC	AAG	AAT	CCT	GAA		239
Gly	Pro	Ala	Ala	Phe	Trp	Leu	Leu	Leu	Phe	Leu	Leu	Lys	Asn	Pro	Glu .		
	65					70					75			٠			
			100						•								
			GCT														287
Ala	Leu	Ala	Ala	Val	Arg	Gly	Glu	Leu	Glu	Ser	Ile	Leu	Trp	Gln	Ala		
80				:	85				7.5	90				. 1	95		1
			GTC													3.	335
Glu	Gln	Pro	Val		Gln	Thr	Thr	Thr		Pro	Gln	Lys	Val	Leu	Asp	- 1	4.25
				100		42	3 -		105					110			7
7				. 5		*-					٠.,						
			GTG														383;
Ser	Thr	Pro	Val	Leu	Asp	Ser	Val		Ser	Glu	Ser	Leu		Leu	Thr		
	٠.		115					120					125		· ·		
		11.0															
			TTC														431
Ala	Ala		Phe	He	Thr	Arg		val	vai	vaı	Asp			Met	Pro		
		130					135					140					
3 m/a	201		000	202	G	mma	220	ama	CON	com	dam	020	000	ama	CTC		400
																	479
met		Asp	GTÀ	Arg	GIU			ьеu	Arg	Arg		Asp	Arg	Lieu	Leu		
	145			٠		150					155						
CmC	mmo	aaa	TTC	CTC.	N.C.C	aaa	CAC	NCN.	. dag	CCN	CNA	A TO	TO	707	CAC .		F 2 F
			Phe														527
160	FILE	PIO	rne	neu	165	FIO	GIII	wrd	мвр	170	GIU	TIE	TAT	THE	175		
100					103					1,0					±13		
CCA	GAG	GTA	TTT	444	тъс	AAC	CGA	שייוירי	CTG	AAC	CCT	GAC	GGA	ፐርኦ	GAG.		575 -
			Phe														3/5
				180		,	5	,	185				1	190			
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AAĠ	AAA	GAC	TTT	TAC	AAG	GAT	GGG	AAA	CGG	CTG	AAG	AAT	TAC	AAC	ATG		623
			Phe														
			195				- "	200				54	205				
			3.5											100	1.0		
			GCG														671
Pro	Trp	210	Ala	GIA	His	Asn	11S	Cys	Leu	GLY	Arg	ser	Tyr	Ala	Val	٠,	
		210			- '		215		14			220					
AAC	AGC	ATC	AAA	CAA	ттт	GTG	TTC	CTT	GTG	CTG	GTG	CAC	TTG	GAC	TTG		719
															Leu		
	225					230					235						
													٠.				
			AAC														767
G1u 240	Leu	ile	Asn	Ala	Asp	vai	GIU	11e	Pro	.250		Asp	Leu	ser	Arg 255		
240					245					250					235 .		
TAC	GGC'	TTC	GGT	CTG	ATG	CAG	CCG	GAA	CAC	GAC	GTG	CCC	GTC	CGC	TAC		815
			Gly														
- 1	. 7		, ī	260					265					270			
			4												15		×
			CCA	TGA	CACA	GGG I	AGCA	JATG(	GA T	CCAC	GTGC'	r cc	CCTC	rgcc			867
Arg	TIE	Arg	Pro 275			1.										,	
			.213		-					6							
CAG	CCTG	CCC /	CAGC	CTGC	cc c	AGCC'	rccc.	A GC	TTTC	TGTG	TGC	ACAG'	TTG (	GCCC	GGGTGC	1.1	927
			1														4
AGG"	TGCT	AGC .	ATTA	CCAC'	TT C	CCTG	TTTT:	r ÇT	CCCA	JAAG	GÇT	GGGT(	CCA (	GGGG.	AGGGAA		987
													1	4			112
AAG	CTAA	JAG (	GGTG	AACA	AA G	AAAA	JACA'	r TG.	AAAG	CTCT	ATG	JA'I'I'	ATC	CACT	GCAAAG	1	047
didada di	DC TOTO	TCC	ממממ	TYPAC	יים חיי	TTYZTY	מדונות מ	r - cc	ידממי	TCAC	ciarco.	מחדב	OTC :	TCAC	CTCGTG	,	107
										,	010			10119			
ATA	TCCA	CAA .	ATGC'	TATT	CA G	ATAA	GGCA	G AA	CTAG	GAGT	CTT	CACT	GCT	CTGC	CCCCAA	1	167
٠.			0	100													
CTC	CCGG	AGG	TGTC.	ACCT	IC C	TAGT	TCTT.	A TG	AGCT.	AGCA	TGG	CCCG	GGC	CTTA	TCCAGT	1	227
													7 17,				
CAA	AGCG	ΑT	GCTG	GCCA	CA G	AAAG	<b>GCCA</b>	C TC	AGGA,	IGÍC	CTT	rulg	TCC .	ATCG.	ATGTCG	. 1	287
ACT	CGAG	TC .										"				1	296
	- 51.0				٠.						•						

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 275 amino acids
  - (B) TYPE: amino acid (D) TOPOLOGY: linear
- and the second s
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu Leu 1 10 15

Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu Glu 20 25 30

Ser	Tyr	Leu 35	Leu	His	Leu	Glu	G1u 40	Met	Gly	Val	Ser	Glu 45	Glu	Met	Gln
Ala	Arg 50	Ala	Leu	Val	Leu	Gln 55	Leu	Trp	Ala	Thr	Gln 60	Gly	Asn	Met	Gly
Pro 65	Ala	Ala	Phe	Trp	Leu 70	Leu	Leu	Phe	Leu	Leu 75	Lys	Asn	Pro	Glu	Ala 80
Leu	Ala	Ala	Val	Arg 85	Gly	Glu	Leu	Glu	Ser 90	lle	Leu	Trp	Gln	Ala 95	Glu
31n	Pro	Val	Ser 100	Gln	Thr	Thr	Thr	Leu 105	Pro	Gln	Lys	Va.1	Leu 110	Asp	Ser
Thr	Pro	Val 115	Leu	Asp	Ser	Val	Leu 120	Ser	Ģlu	Ser	Ļeu	Arg 125	Leu	Thr	Ala
Ala	Pro 130	Phe	Ile	Thr	Arg	Glu 135	Val	Val	Val	Asp	Leu 140	Ala	Met	Pro	Met
Ala 145	Asp	Gly	Arg	Glu	Phe 150		Leu	Arg	Arg	Gly 155	Asp	Arg	Leu	Leu	Leu 160
Phe	Pro	Phe	Leu	Ser 165	Pro	Gln	Arg	Asp	Pro 170	Glu	Ile	Tyr	Thr	Asp 175	Pro
Glu	Val	Phe	Lys 180	Tyr	Asn	Arg	Phe	Leu 185	Asn	Pro	Asp	Gly	Ser 190	Glu	Lys
Lys	Asp	Phe 195		Lys	Asp	Gly	Lys 200	Arg	Leu	Lys	Asn	Tyr 205	Asn	Met	Pro
	Gly 210	Ala	Gly	His	Asn	His 215	Cys	Leu	Gly	Arg	Ser 220	Tyr	Ala	Val	Asn
Ser 225		Lys	Gln	Phe	Val 230	Phe	Leu	Val	Leu	Val 235	His	Leu	Asp	Leu	Glu 240
Leu	Ile	Asn	Ala	Asp 245	Val	Glu	Ile	Pro	Glu 250	Phe	Asp	Leu		Arg 255	Tyr
Gly	Phe		Leu 260	Met	Gln	Pro	Glu	His 265	Asp	Val	Pro	Val	Arg 270	Tyr	Arg
Ile	Arg	Pro 275		. 30						1					

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1977 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

	(V1)	ORĮ	GINA	T SO	URCE	s: .												
		. (A	OF	GANI	SM:	Homo	sap	iens										
	(ix)	FEA	TURE	3:														
		(A	) NA	ME/K						-								
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	(ix)	FEA	TURE	3:														
	, , , , ,			WE\K	EY:	mat_	pept	ide										
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Gly	Tyr	Ala	Leu	Asp 45	Phe	GIY	Lys	Asp	Ala 50	Ala	Ser	Phe	Leu	Thr 55				
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Met	Lys	Glu	Lys	His	Gly	Asp	Ile		Thr	Ile	Leu	Val	Gly.	Gly	Arg			
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Tyr			Val	Leu	Leu	Asp		His	Ser	Tyr	Asp	Ala	Val-	Val	Trp			
		75				-	80					. 85		·				
									GCC								. 33	9
Glu		Arg	Thr	Arg	Leu		Phe	His	Ala	Tyr		Ile	Phe	Leu	Met			
	90					95					100							
GAG	AGG	ATT	TTT	GAT	GTG	CAG	CTT	CCA	CAT	TAC	AGC	ccc	AGT	GAT	GAA		38	37
	Arg	Ile	Phe			Gln	Leu	Pro	His			Pro	Ser	Asp				
105					110					115		٠.			120		- 5	
AAG	GCC	AGG	·ATG	AAA	CTG	ACT	CTT	CTC	CAC	AGA	GAG	CTC	CAG	GCA	CTC		43	35
Lys	Ala	Arg	Met	Lys	Leu	Thr	Leu	Leu	His	Arg	Glu	Leu	Gln	Ala	Leu			
				125					130					135				
ACA	GAA	GCC	ATG	TAT	ACC	AAC	CTC	CAT	GCA	GTG	CTG	TTG	GGC	GAT	GCT		. 48	33
									Ala									
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MOLECULE TYPE: cDNA

Thr Glu Ala G	ly Ser Gly Trp	His Gl	u Met Gly	Leu Leu	Asp Phe	Ser
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	TAC	AGC	TTC	CTG-	CTC	AGA	GCC	GGC	TAC	CTG	ACT	CTT	TAC	GGA	ATT	GAG		579	
														Gly				0.5	
		170					175		-2-			180		1					
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	GCG	CTG	CCA	CGC	ACC	CAT	GAA	AGC	CAG	GCC	CAG	GAC	CGC	GTC	CAC	TCA		627	
	Ala	Leu	Pro	Arg	Thr	His	Glu	Ser	Gln	Ala	Gln	Aşp	Arg	Val	His	Ser			
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	Leu	Trp	Ala	Thr	Gln	Gly	Asn	Met	Gly	Pro	Ala	Ala	Phe	Trp	Leu	Leu	1111		
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														CGC			,	963	
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														Gln				1011	
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	ACT	CTC	CCA	CAG	AAG	GTT	CTA	GAC	AGC	ACA	CCT	GTG	CTT	GAT	AGC	GTG		1059	
	Thr	Leu	Pro	Gln	Lys	Va1	Leu	Asp	Ser	Thr	Pro	Val	Leu	Asp	Ser	Val			
		330		. 1		. 1	335			10		340							
														ACC.				1107	
		Ser	Glu	ser			Leu	Thr	Ala	Ala		Phe	Ile	Thr	Arg	Glu			
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				GAC													1299
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423					430			. "		.433	b				440		
TGC	CTG	GGG	AGG	AGT	тат	GCG	GTC	AAC	AGC	ATC	AAA	CAA	ффф	GTG	TTC		1395
															Phe		1333
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CTT	GTG	CTG	GTG	CAC	TTG	GAC	TTG	GAG	CTG	ATC	AAC	GCA	GAT	GTG	GAG	7	1443
Leu	Val	Leu	Val	His	Leu	Asp	Leu	Glu	Leu	Ile	Asn	Ala	Asp	Val	Glu		
7.	· ·		460	5 -				465					470				
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Ile	Pro			Asp	Leu	Ser		Tyr	Gly	Phe	Gly		Met	Ģln	Pro		
		475			· .		480	:	*			485					1 - 1
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dan	mmam	ama i	maar	aram.		aaaa	aama		amaa	mraa	a mm		amm	aaam	GCTTT	m i	1650
GCI	TICI	GIG	IGCA	CAGT	16 6	CCCG	5616	C AG	GIGC	IAGC	ALL	ACCA	CIT	ccci	GCTTT	1	1657
СТС	CCAG	AAG (	GCTG	GGTC	CA G	GGGĄ	GGGA	AA A	GCTA	AGAG	GGT	GAAÇ.	AAA	GAAA	AGACA	T	1717
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IGA	MAGC	101	AIGG	VÍTV	10, 0	ACIG	cana	GIL	1141	iicc	inna	ni ch	GGC.	1110	icide	- · ·	LIII.
ccc	TTAA	CAC	CTCG	TTAC	TC T	ĊACC	TCGT	G AT	ATCC	ACAA	ATG	CTAT	TCA	GATA	AGGCA	G.	1837
AAC	TĄGG	AGT	CTTC	ACTG	CT C	TGCC	CCCA	А СТ	CCCG	GAGG	TGT	CACC	TTC	CTAG	TTCTT	A	1897
TGA	GCTA	GCA	TGGC	CCGG	GC C	TTAT	CCAG	T CA	AAGC	GGAT	ĢCT	GGCC	ACA	GAAA	GGCCA	С	1957
TCA	GGAT	GTC	CŢTT	GTGT	CC										į, ž		1977

# (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 500 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

- Met Ala Trp Ala Ala Leu Leu Gly Leu Leu Ala Ala Leu Leu Leu Leu 1 5 10 15
- Leu Leu Ser Arg Arg Thr Arg Arg Pro Gly Glu Pro Pro Leu
- Asp Leu Gly Ser Ile Pro Trp Leu Gly Tyr Ala Leu Asp Phe Gly Lys
- Asp Ala Ala Ser Phe Leu Thr Arg Met Lys Glu Lys His Gly Asp Ile 50 60
- Phe Thr Ile Leu Val Gly Gly Arg Tyr Val Thr Val Leu Leu Asp Pro 65 70 75 80
- His Ser Tyr Asp Ala Val Val Trp Glu Pro Arg Thr Arg Leu Asp Phe 85 90 95
- His Ala Tyr Ala Ile Phe Leu Met Glu Arg Ile Phe Asp Val Gln Leu 100 105 110
- Pro His Tyr Ser Pro Ser Asp Glu Lys Ala Arg Met Lys Leu Thr Leu 115 120 125
- Leu His Arg Glu Leu Gln Ala Leu Thr Glu Ala Met Tyr Thr Asn Leu 130 135 140
- His Ala Val Leu Leu Gly Asp Ala Thr Glu Ala Gly Ser Gly Trp His 145 150 155 160
- Glu Met Gly Leu Leu Asp Phe Ser Tyr Ser Phe Leu Leu Arg Ala Gly 165 170 175
- Tyr Leu Thr Leu Tyr Gly Ile Glu Ala Leu Pro Arg Thr His Glu Ser 180 185 190
- Gln Ala Gln Asp Arg Val His Ser Ala Asp Val Phe His Thr Phe Arg 195 200 205
- Gln Leu Asp Arg Leu Leu Pro Lys Leu Ala Arg Gly Ser Leu Ser Val 210 215 220
- Gly Asp Lys Asp His Met Cys Ser Val Lys Ser Arg Leu Trp Lys Leu 225 230 235 240
- Leu Ser Pro Ala Arg Leu Ala Arg Arg Ala His Arg Ser Lys Trp Leu \$245\$
- Glu Ser Tyr Leu Leu His Leu Glu Glu Met Gly Val Ser Glu Glu Met 260 265 270
- Gln Ala Arg Ala Leu Val Leu Gln Leu Trp Ala Thr Gln Gly Asn Met 275 280 285
- Gly Pro Ala Ala Phe Trp Leu Leu Leu Phe Leu Leu Lys Asn Pro Glu 290 295 300

Ala Leu Ala Ala Val Arg Gly Glu Leu Glu Ser Ile Leu Trp Gln Ala 305 310 315

Glu Gln Pro Val Ser Gln Thr Thr Leu Pro Gln Lys Val Leu Asp 325 330 335

Ser Thr Pro Val Leu Asp Ser Val Leu Ser Glu Ser Leu Arg Leu Thr 340 345 350

Ala Ala Pro Phe Ile Thr Arg Glu Val Val Val Asp Leu Ala Met Pro 355 360 365

Met Ala Asp Gly Arg Glu Phe Asn Leu Arg Arg Gly Asp Arg Leu Leu 370 380

Leu Phe Pro Phe Leu Ser Pro Gln Arg Asp Pro Glu Ile Tyr Thr Asp 385 390 395

Pro Glu Val Phe Lys Tyr Asn Arg Phe Leu Asn Pro Asp Gly Ser Glu 405 410 415

Lys Lys Asp Phe Tyr Lys Asp Gly Lys Arg Leu Lys Asn Tyr Asn Met

Pro Trp Gly Ala Gly His Asn His Cys Leu Gly Arg Ser Tyr Ala Val
435 440 445

Asn Ser Ile Lys Gln Phe Val Phe Leu Val Leu Val His Leu Asp Leu 450 455 460

Glu Leu Ile Asn Ala Asp Val Glu Ile Pro Glu Phe Asp Leu Ser Arg 465 470 475 480

Tyr Gly Phe Gly Leu Met Gln Pro Glu His Asp Val Pro Val Arg Tyr 485 490 495

Arg Ile Arg Pro

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"

### (xi) SEQUENCE DESCRIPTION: SEO ID NO:16:

- (2) INFORMATION FOR SEQ ID NO:17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 24 base pairs
    - (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: other nucleic acid
    - (A) DESCRIPTION: /desc = "PRIMER/SYNTHETIC DNA"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGTGTGGCC CACAGCTGCA GCAC

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